

Supplementary table S1: NCBI accession numbers and names of genomes in the study

S.No.	NCBI accession number and name
1.	MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
2.	MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
3.	MN975262.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-005b_2020, complete genome
4.	MN985325.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV/USA-WA1/2020, complete genome
5.	MN988713.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV/USA-IL1/2020, complete genome
6.	MN994467.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV/USA-CA1/2020, complete genome
7.	MN994468.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV/USA-CA2/2020, complete genome
8.	MN997409.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV/USA-AZ1/2020, complete genome
9.	MN988668.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV WHU01, complete genome
10.	MN988669.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV WHU02, complete genome
11.	MN996527.1 Severe acute respiratory syndrome coronavirus 2 isolate WIV02, complete genome
12.	MN996528.1 Severe acute respiratory syndrome coronavirus 2 isolate WIV04, complete genome
13.	MN996529.1 Severe acute respiratory syndrome coronavirus 2 isolate WIV05, complete genome
14.	MN996530.1 Severe acute respiratory syndrome coronavirus 2 isolate WIV06, complete genome
15.	MN996531.1 Severe acute respiratory syndrome coronavirus 2 isolate WIV07, complete genome
16.	NC_003436.1 Porcine epidemic diarrhea virus, complete genome
17.	NC_002645.1 Human coronavirus 229E, complete genome
18.	NC_005831.2 Human Coronavirus NL63, complete genome
19.	NC_002306.3 Feline infectious peritonitis virus, complete genome
20.	NC_006577.2 Human coronavirus HKU1, complete genome
21.	NC_001846.1 Mouse hepatitis virus strain MHV-A59 C12 mutant, complete genome
22.	NC_003045.1 Bovine coronavirus, complete genome
23.	NC_001451.1 Avian infectious bronchitis virus, complete genome
24.	NC_004718.3 SARS coronavirus, complete genome
25.	NC_009021.1 Bat coronavirus HKU9-1, complete genome
26.	NC_009019.1 Bat coronavirus HKU4-1, complete genome
27.	NC_009657.1 Scotophilus bat coronavirus 512, complete genome
28.	NC_010646.1 Beluga Whale coronavirus SW1, complete genome
29.	NC_009020.1 Bat coronavirus HKU5-1, complete genome
30.	NC_009988.1 Bat coronavirus HKU2, complete genome

31.	NC_010437.1 Bat coronavirus 1A, complete genome
32.	NC_010438.1 Bat coronavirus HKU8, complete genome
33.	NC_010800.1 Turkey coronavirus, complete genome
34.	NC_012936.1 Rat coronavirus Parker, complete genome
35.	NC_017083.1 Rabbit coronavirus HKU14, complete genome
36.	NC_018871.1 Rousettus bat coronavirus HKU10, complete genome
37.	NC_019843.3 Middle East respiratory syndrome coronavirus, complete genome
38.	NC_022103.1 Bat coronavirus CDPHE15/USA/2006, complete genome
39.	NC_023760.1 Mink coronavirus strain WD1127, complete genome
40.	NC_025217.1 Bat Hp-betacoronavirus/Zhejiang2013, complete genome
41.	NC_026011.1 Betacoronavirus HKU24 strain HKU24-R05005I, complete genome
42.	NC_028752.1 Camel alphacoronavirus isolate camel/Riyadh/Ry141/2015, complete genome
43.	NC_028806.1 Swine enteric coronavirus strain Italy/213306/2009, complete genome
44.	NC_028824.1 BtRf-AlphaCoV/YN2012, complete genome
45.	NC_028811.1 BtMr-AlphaCoV/SAX2011, complete genome
46.	NC_028814.1 BtRf-AlphaCoV/HuB2013, complete genome
47.	NC_028833.1 BtNv-AlphaCoV/SC2013, complete genome
48.	NC_030292.1 Ferret coronavirus isolate FRCoV-NL-2010, complete genome
49.	NC_030886.1 Rousettus bat coronavirus isolate GCCDC1 356, complete genome
50.	NC_032107.1 NL63-related bat coronavirus strain BtKYNL63-9a, complete genome
51.	NC_032730.1 Lucheng Rn rat coronavirus isolate Lucheng-19, complete genome
52.	NC_034972.1 Coronavirus AcCoV-JC34, complete genome
53.	NC_035191.1 Wencheng Sm shrew coronavirus isolate Xingguo-101 ORF1ab polyprotein, spike glycoprotein, envelope protein, membrane protein, and nucleocapsid protein genes, complete cds
54.	NC_039207.1 Betacoronavirus Erinaceus/VMC/DEU/2012 isolate ErinaceusCoV/2012-174/GER/2012, complete genome
55.	NC_038294.1 Betacoronavirus England 1, complete genome
56.	NC_038861.1 Transmissible gastroenteritis virus complete genome, genomic RNA
57.	NC_006213.1 Human coronavirus OC43 strain ATCC VR-759, complete genome
58.	NC_045512.2 Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome

Supplementary file S2: Primer3 result file showing alignment and properties of the primers

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PRIMER PICKING RESULTS FOR COVID-19 Target Seq 1
No mispriming library specified
Using 0-based sequence positions
SEQUENCE SIZE: 503
INCLUDED REGION SIZE: 503

TARGETS (start, len)*: 200,103
PAIR_OK_REGIONS (left_start, left_len, right_start, right_len)*: 0,200,303,200
 0 aggaattttatgaaccacaatcattactacagacaacacatttctgctgtaactgt
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>

 60 gatgttgtaataggaattgtcaacaacacagtttatgatcctttgcaacctgaattagac
      >>>>>>>

120 tcattcaaggaggagtagataaatattttaagaatcatatcaccagatgttgattta

180 ggtgacatctctggcattaatgcttcagttgtaaaccattcaaaaagaaattgaccgcctc
      *****

240 aatgaggttgccaagaatttaaatgaatctctcatcgatctccaagaacttgaaaagtat
      *****

300 gagcatatataaaatggcatggtacatttgctgtagttttatagctggttgaattgcc
      ***

360 atagtaatggtgacaattatgctttgctgtatgaccagttgctgtagttgctcaagggc

420 tgtttgctctgtagcctgtgcaatttgatgaagacgactctgagccagctcaaaa
      <<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<

480 ggagtcaaattacattacacata

KEYS (in order of precedence):
***** target
>>>>> left primer
<<<<<<< right primer
^^^^^^ left primer / right primer overlap

1 LEFT_PRIMER      start  len    tm     gc%  any_th  3'_th hairpin seq
                   44    23    58.87  43.48  0.00    0.00   36.78 tgtatctgtaactatgatotta

1 RIGHT_PRIMER     start  len    tm     gc%  any_th  3'_th hairpin seq
                   444    19    58.93  52.63  15.82   0.00   0.00  tgcagcaggatccacaaga
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Supplementary file S3: FASTA file of all predicted PCR products across all genomes of SARS-CoV 2 and SARS-CoV 1.

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ATTCAAGGAGGAGTTAGATAAATATTTTAAGAATCATACATCACCAGATGTTGAT
TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTTAAACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGGAAGTATGAGCAGTATATAAAATGGCCATGGTACATTGGCTAGGTTTT
ATAGCTGGCTTGATTGCCATAGTAATGGTGACAATTATGCTTTGCTGTATGACCA
GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN938384.1      fpdiffs=0(match) rpdiffs=0(match)  Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
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ATTCAAGGAGGAGTTAGATAAATATTTTAAGAATCATACATCACCAGATGTTGAT
TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTA AACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
ATAGCTGGCTTGATTGCCATAGTAATGGTGACAATTATGCTTTGCTGTATGACCA
GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN996531.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate WIV07, complete genome

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ATTCAAGGAGGAGTTAGATAAATATTTTAAGAATCATACATCACCAGATGTTGAT
TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTA AACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
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GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN994467.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate 2019-nCoV/USA-CA1/2020, complete genome

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ATTCAAGGAGGAGTTAGATAAATATTTTAAGAATCATACATCACCAGATGTTGAT
TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTA AACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
ATAGCTGGCTTGATTGCCATAGTAATGGTGACAATTATGCTTTGCTGTATGACCA
GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN996528.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate WIV04, complete genome

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ATTCAAGGAGGAGTTAGATAAATATTTTAAGAATCATACATCACCAGATGTTGAT
TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTA AACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
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>MN996529.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate WIV05, complete genome

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TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTA AACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
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GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN988668.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate 2019-nCoV WHU01, complete genome

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ATTCAAGGAGGAGTTAGATAAATATTTTAAGAATCATACATCACCAGATGTTGAT
TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTA AACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT

ATAGCTGGCTTGATTGCCATAGTAATGGTGACAATTATGCTTTGCTGTATGACCA
GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN997409.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate 2019-nCoV/USA-AZ1/2020, complete genome

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TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTAACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
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>MN988713.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate 2019-nCoV/USA-IL1/2020, complete genome

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TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTAACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
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GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN975262.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-005b_2020, complete genome

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TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTAACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
ATAGCTGGCTTGATTGCCATAGTAATGGTGACAATTATGCTTTGCTGTATGACCA
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>MN988669.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate 2019-nCoV_WHU02, complete genome

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ATTCAAGGAGGAGTTAGATAAATATTTTAAGAATCATACATCACCAGATGTTGAT
TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTAACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
ATAGCTGGCTTGATTGCCATAGTAATGGTGACAATTATGCTTTGCTGTATGACCA
GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN908947.3 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

TAATAGGAATTGTCAACAACACAGTTTATGATCCTTTGCAACCTGAATTAGACTC
ATTCAAGGAGGAGTTAGATAAATATTTTAAGAATCATACATCACCAGATGTTGAT
TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTAACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
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GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN996530.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate WIV06, complete genome

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ATTCAAGGAGGAGTTAGATAAATATTTTAAGAATCATACATCACCAGATGTTGAT
TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTA AACATTCAAAAAGAAATTG
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ACTTGGAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
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>MN985325.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate 2019-nCoV/USA-WA1/2020, complete genome

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TTAGGTGACATCTCTGGCATTAAATGCTTCAGTTGTA AACATTCAAAAAGAAATTG
ACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATCGATCTCCAAGA
ACTTGGAAGTATGAGCAGTATATAAAATGGCCATGGTACATTTGGCTAGGTTTT
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GTTGCTGTAGTTGTCTCAAGGGCTGTTGT

>MN994468.1 fpdiffs=0(match) rpdiffs=0(match) Severe acute respiratory
syndrome coronavirus 2 isolate 2019-nCoV/USA-CA2/2020, complete genome

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syndrome coronavirus 2 isolate WIV02, complete genome

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GTTGCTGTAGTTGTCTCAAGGGCTGTTGT